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STIC-Biotec From: Sent: T : Subject:	Friday, November 08, 2002 1:18 PM STIC-Biotech/ChemLib Sequence search	
/ Could you pleas	se do an oligomer search of Serial number 09/918026 (SEQ ID	NO: 3)
2 · Please do a len SAND or RAS Terra Gibbs AU 1635 / Mailbox 11E 306-3221	#79523 E12	
Dear M.	o. Gibbs	Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 793-308-3634
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Searcher Prep/Review:	Full text:	Sequence Sys.:
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Title: US-09-918-026A-3
Perfect score: 1569

Sequence: l atggagccaggcggggcccg.......cttggtcctgccatacctag 1569
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 2054640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

mbl:* b_ba:* b_ba:* b_ln:* b_ln:* b_ln:* b_lom:* b_pow:* b_pow	htgo htgo htgo
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Pred. No. is the number of results predicted by chance to have a

F331502S04 100 bp DNA linear PRI 13-MAR-2001 Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,

AF331505 AF331505.1 GI:13310366

ACCESSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM

REFERENCE AUTHORS

exon 4

RESULT 1 F331502S04 LOCUS DEFINITION

ALIGNMENTS

4 of 15
Homo sapiens.
Homo sapiens
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Eukaria (Craniata; Vertebrata; Euteleostomi;
Bukaria; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,

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                                                                                                             Submitted (22-DEC-2000) Department of Pediatrics, Faculty of Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F331502S02 96 bp DNA linear PRI 13-MAR-2001
Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
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I (bases I to 90.

Katsuren, K., Tamura, T., Arashiro, R., Takata, K., Matsuura, T., Niikawa, N. and Ohta, T.

Structure of the human acyl-CoA:cholesterol acyltransferase-2

CACAT-2) gene and its relation to dyslipidemia
                                                                                                                                                                                                                                                                                                                                                        Gaps
       Structure of the human acyl-CoA:cholesterol acyltransferase-2 (ACAT-2) gene and its relation to dyslipidemia Unpublished
                                                                                                                                                                                                                                                                                                                               Gaps
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Niikawa,N. and Ohta,T.
Direct Submission
                                                     2 (bases 1 to 100)
Katsuren. K., Tamura, T., Arashiro, R., Takata, K., Matsuura, T.
Niisawa, N. and Ohta, T.
Direct Submission
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                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                 4.0%; Score 63; DB 9; Le ilarity 100.0%; Pred. No. 5.6e-24; Conservative 0; Mismatches 0;
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                                                                                                                                                                               /organism="Homo saplens"
/db_xref="taxon:9606"
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/orqanism="Homo
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AF331503.1 GI:13310364
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Niikawa, N. and Ohta, T.
                                                                                                                                                                                                                          /gene="SOAT2"
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25 c
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27 c
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Best Local Similarity 100.
Matches 58; Conservative
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                                                                                                                                           903-0125, Japan
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Best Local
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Ratsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,
Nilkawa,N. and Ohta,T.
Direct Submission
Submitted (12-DEC-2000) Department of Pediatrics, Faculty of
Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
                                                                                                                                              #331DU2SO7 100 bp DNA linear PRI 13-MAR-2001
Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
exon 7.
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AF331516.1 GI:13310377
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 90)

Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,

Niikawa,N. and Ohta,T.
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T., Niikawa,N. and Ohta,T. Structure of the human acyl-CoA:cholesterol acyltransferase-2 (ACAT-2) gene and its relation to dyslipidemia Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure of the human acyl-CoA:cholesterol acyltransferase-2 (ACAT-2) gene and its relation to dyslipidemia upublished 2 (bases I to 90) (bases I to 90) (k. Tanura, R., Tanura, T., Arashiro, R., Takata, N. and Ohta, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
706 CAGGTTAGGTTCCTGATGAAAAGCTACTCCTTCCTGAGAGAGGCTGTGCCTGGGA 760
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100.0%; Pred. No. 2.2e-19;
ative 0; Mismatches 0;
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1. 100
/organism="Homo sapiens"
/db_xref="taxon:9606"
16. 85
/gene="SOAT2"
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AF331508.1 GI:13310369
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Homo sapiens
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Matches 55; Conserv
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TITLE JOURNAL

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 91)

S Katsuren, K., Tamura, T., Arashiro, R., Takata, K., Matsuura, T., Niikawa, N. and Ohta, T.

Structure of the human acyl-CoA:cholesterol acyltransferase-2 (ACAT-2) gene and its relation to dyslipidemia

L Unpublished

E 2 (bases 1 to 91)

S Katsuren, K., Tamura, T., Arashiro, R., Takata, K., Matsuura, T., Niikawa, N. and Ohta, T.

Direct Submission

L Submitted (22-DEC-2000) Department of Pediatrics, Faculty of Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sandluolo,F., Bruscia,E., Capon,F. and Novelli,G.
Fine mapping of muscular dystrophy with rimmed vacuoles (MDVR)
using 11 novel microsatellite markers from chromosome 19pl3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (31-MAR-2000) Sangiuolo F., Biopathology, To
University, via di Tor Vergata 135, 00133 Rome, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; ... 6.1e-16; 0; Indels
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Pred. No. 6.16
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/chromosome="19"
/map="19p13.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32. .47 /evidence=experimental
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/rpt_unit=79. .85
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/gene="SOAT2"
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Matches 49; Conservative
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Unpublished
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AF331504.1:21. 157, AF331505.1:21. 80, AF331506.1:21. 128,
AF331507.1:16. 280, AF331508.1:16. 188, AF331509.1:16. 1100,
AF331510.1:21. 66, AF331511.1:21. 150, AF331512.1:21. 118,
AF331513.1:16. 114, AF331514.1:21. 156, AF331515.1:16. 161,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="acyl-coA:cholesterol acyltransferase-2"

join(AF331502.1:21. .102.AF331503.1:21. .76,

AF331504.1:21. .157,AF331505.1:21. .80,AF331506.1:21. .128,

AF331510.1:16. .280,AF331508.1:16. .85,AF331509.1:16. .100,

AF331510.1:21. .66,AF331511.1:21. .150,AF331512.1:21. .118,

AF331513.1:16. .114,AF331514.1:21. .156,AF331515.1:16. .161
Direct Submission
Submitted (22-DEC-2000) Department of Pediatrics, Faculty of
Medicine, University of the Ryukyus, 207 Uchara, Nishihara, Okinawa
903-0125, Japan
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/protein_id="AAK18275.1"
/db_xref="G1:13310378"
/translation="MEPGRAILIQRTEGIGGERERQPCGDGNTETHRAPDLVQWTRH
MEAVRAQLIEGOAGGILELIDRAMREAIQSYPSQDKFLPPPPPGSLSRTQEPSGIGKQK
VFIIRKSLLDELMEVQHFRIIYHMFIAGLCVFIISTLAIDFIDEGRILLIEFDLLIFSF
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AVEHQLPPASRCVLVFEQVRFLMKSYSFLREAVPGTLRARRGEGIQAPSFSSYLYFLF
CPTLIYRETYPRTPYVRWNYVAKNFAQALGCVLYACFILGRLCVPVFANMSREPFSTR
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TWNVVVHDWLYSYVYQDGLRLLGARARGVAMLGVFLVSAVAHEYIFCFVLGFFYPVML
ILFLVIGGMLNFMMHDQRTGPAWNVLMWTMLFLGQGIQVSLYCQEWYARRHCPLPQAT
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Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
exon 9.
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/dL_xref="taxon:9606"

order_AR31504.1:1..177,AF331505.1:1..100,AF331506.1:1..148,

AF331504.1:1..295,AF331508.1:1..100,AF331506.1:1..115,

AF331501.1:1..91,AF331511.1:1..170,AF331512.1:1..38,

AF331511.1:1..129,AF331511.1:1..176,AF331515.1:1..176,
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PAT 07-SEP-2001
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Identification of the dombrock blood group glycoprotein as a polymorphic member of the adp-ribosyltransferase gene family Patent: WO 0233084-A 71 25-APR-2002;
NEW YOR BLOOD GT (US); GOVERNMENT OF THE UNITED STATES (US) NEW YOR Location/Qualifiers
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 Length 20;
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synthetic construct
artificial sequences.
1 (bases 1 to 25)
Luche, R.M. and Wei, B.
Dsp-12 and dsp-13 dual specificity phosphatases
Patent: Wo 0157221-A 16 09-AUG-2001;
Coeptyr, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 1.9e+04;
tive 0; Mismatches 0;
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1.0%; Score 15; DB 6; L. 100.0%; Pred. No. 1.8e+04; ative 0; Mismatches 0;
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/organism="synthetic construct"
/db_xref="taxon:32630"
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Sequence 71 from Patent WO0233084.
AX428505
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Sequence 16 from Patent W00157221.
AX223975 41:15551642

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    /organism="synthetic c
/db_xref="taxon:32630"
/note="Primer"

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                                                                                                                                                                                                                                      Masakazu,M., Kazumasa,H., Kenichi,O. and Masashi,M. Mazakazu,M., Kazumasa,H., Kenichi,O. and Masashi,M. Method for the type classification of hepatitis B viruses and primer and probe to be used therein Patent: JP 1999103898-A 14 20-APR-1999;
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/organism='Unidentified'
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"
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Antisense modulation of ptplb expression
Patent: WO 0210378-A 174 07-FEB-2002;
ISIS PHARMACEUTICALS, INC. (US)
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Sequence 174 from Patent WO0210378.
AX418779
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    /organism="unidentified"
    /db_xref="taxon:32644"

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JP 1999103898-A/14
20-APR-1999
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JP 1999103898-A/14.
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9
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100.0%; Pred. No. 1.9e+04;
iive 0; Mismatches 0;
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Sequence 28 from Patent W00220786.
AX398736
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/db_xref="taxon:32644"
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                                        E30087

Human BMP-7 promoter and method for detecting bone-associated substance by using the same Human BMP-7 promoter and method for detecting bone-associated substance by using the same.
                                                                                                                                                                                                                                                                                                                                               SHINJI KAWAI, TAKEYUKI SUGIURA
CIZAL5/09, CI2N5/10, CI2Q1/68//A61K48/00, (C12N5/10, C12R1:91), PC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Cargill, M., Ireland, J. S. and Lander, E. S.
Human single nucleotide polymorphisms
Patent: WO 0166800-A 13-SEP-2001,
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
                                                                                                                                                                                        Shinji,K. and Takeyuki,S. Human BMP-7 promoter and method for detecting bone-associated substance by using the same Patent: JP 1999313675-A 2 16-NOV-1999; HOECHST MARION ROUSSEL GMBH
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Sequence 4 from Patent W00166800.
AX247925
AX247925.1 GI:15862548
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1 9 c 7 g 6
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C12N5/00,(C12N5/00,C12R1:91)
Strandedness: Single;
Topology: Linear;
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/organism="unidentified"
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JP 1999313675-A/2
16-NOV-1999
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Matches 15; Conservative
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PAT 27-MAY-2002
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Tullin, S. and Kasper, A.
A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
INFLUENCE ON A CELLULAR RESPONSE
Patent: WO 9845704-A 106 15-OCT-1998;
TULLIN SOREN (DK); KASPER ALMHOLT (DK)
Location/Qualifiers
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Length 31;
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Kinase d interacting protein
Patent: Wo 0220786-A 28 14-WAR-2002;
IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB)
Location/Qualifiers
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1.0%; Score 15; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 0;
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/db_xref="taxon:32630"
/note="Primer"
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Sequence 106 from Patent WO9845704.
A84491
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                           PAT 18-JUN-2002
                                                                                                                                                          Thastrup,O., Bjoern,S.P., Tullin,S., Almholt,K. and Scudder,K. A method for screening substances for effect on intracellular translocation
Patent: EP 1199564-A 106 24-APR-2002;
Blolmage A/S (DK)
Location/Qualifiers
1. .32
/organism="unidentified"
/db_arref="taxon:32644"
6 a 12 c 9 9 5 t
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Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels
                              DNA
                      32 bp ESquence 106 from Patent EP1199564. AA427390 AX427390.1 GI:21530743
                                                                                                   unidentified.
unidentified
unclassified.
RESULT 15
AA427390/c
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Search completed: November 14, 2002, 20:23:03 Job time : 2877 secs

oy D #13947 for g brain expres

Human Human

Human bone marrow Probe #13125 for g Probe #17401 used Probe #9011 used t Human genome-deriv Human EGF ** target PCR primer #2 from Hepatitis B virus Rat PTPBB antisens Rat PTPBB antisens Rat PTPBB mRNA lev Human Her-1 antise Human SPNA CDNA, P

Porphobilinogen de

Human DSP-12 cDNA

Human aquaporin 5 Primer B13 of the Human BMP-7 exon 1

Human single nucle Rat kidins220 C-te Primer Zap70-botto

A. fumigatus codon Human sFv library Human RING finger

Human insulin codi

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Human silent SNP Human silent SNP

coding

Human

PAFP1-TfeAFP gene

Title: Perfect score:

Sequence:

nucleic

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Run on:

Scoring table:

Minimum DB s Maximum DB s

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New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human spliced transcript detection oligonucleotide SEQ ID NO:9597
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splice variant; transcriptome; oligonucleotide library; ss.
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                                                AA148715
AA109020
ABS16691
AAV97364
AAZ37843
AAX55895
AAD12117
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AAD36657
ABK37361
AAD38835
AAX76655
ABN89782
ABD61310
AAV25385
AAZ55621
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ABK51212
AAV71069
ABK47693
AAT13190
AAD17998
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02-MAY-2001; 2001US-287724P.
20-JUL-2001; 2001WO-IB01903.
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Wasserman
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WO200210449-A2
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ABN36849;
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Human acyl CoA:cho
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Human breast cell
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Human ACAT Related
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                                                                  November 14, 2002, 18:10:46; Search time 254 Seconds (without alignments) 13910.966 Million cell updates/sec
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                                                                                                                                   1 atggagccaggcggggcccg......cttggtcctgccatacctag 1569
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       5.1.3
Compugen Ltd
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                                                                                                                                                                                     2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
        GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                nucleic search, using sw model
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AAA76183
AA257363
AAZ57364
ABN28762
AAZ77373
AAV21372
ABA50541
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Gapop 60.0 , Gapext 60.0
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the obligation is appression profitling studies, in qualitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal characteripts and splice variants of human or animal libraries to detect transcripts of a sub-transcriptome under a particular blological or pathological state, and so allowing the particular blological or pathological state, and so allowing the only expressed in specific tissue under a specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA cranscripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN2753 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the examplification of the present invention.

Seculication, but was obtained in electronic format directly from WIPO
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enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
                                                                   The present invention describes oligonucleotide libraries for detecting
                                                                                messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNAs splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1017 TATCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTCTTTGCCTTCCT 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%; Score 60; DB 24; Length 60
100.0%; Pred. No. 1.9e-18;
tive 0; Mismatches 0; Indels
detecting tissue-, pathology-, and
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60 BP; 7 A; 21 C; 10 G; 22 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                          SEQ ID 9597; 47pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA76178 standard; DNA; 25 BP
              developmental-specific genes
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Best Local Similarity
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Human; ACAT Related Gene Product 2; ARGP2;
enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
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                                                                                                                                      The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates sterol esterification, an important component of intracellular lipid homeostasis. The present invention relates to human ACAT Related Gene Product 2 (ARGP2). ARGP2 is a diacylglycerol acyltransferase (DGAT). ARGP2 is a tissue specific sterol esterification enzyme. The present sequence is a PCR primer used to isolate ARGP2 coding sequence
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useful for treating hyperlipidemia, atherosclerosis, heart disease, other diseases associated with an imbalance of triglyceride levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ACAT Related Gene Product 2 ARGP2 PCR primer 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
0.34;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 BP; 3 A; 8 C; 4 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 9 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Score 24; DB 100.0%; Pred. No. 0.3 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 17; 32pp; English.
                                                                                     Disclosure; Column 17; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1047 CATGCTGCTCATCTTTGC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CATGCTGCTCCTCTTCTTTGC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA76183 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oelkers P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGAT; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-557622/51
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Best Local Similarity
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les 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA76183;
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Matches
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Matches

AAZ57363;

AAZ57363

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The present sequence represents a PCR primer for the human acyl CoA:cholesterol acyltransferase designated ACAT-2. ACAT-2 polypeptides can be administered therapeutically, especially by expressing encoding polynucleotides, to treat individuals in need of ACAT-2 polypeptide. They may especially be administered to treat disease conditions associated with elevated cholesterol ester levels e.g. hyperrolesterolaemia or hyperlipidaemia (including hyperrolesterolaemia), since ACAT-2 catalyses the esterification of cholesterol with fatty acyl CoA substrates. The polypeptides can also be used to diagnose diseases related to polypeptide expression or activity, by analysing for polypeptide presence or amount in a sample. They are useful to screen for compounds inhibiting or activating the polypeptide, which can be included in pharmaceutical compositions and administered therapeutically to treat conditions associated with ACAT-2; inhibitory agents can especially, and especially agents which selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide, useful to treat conditions associated with elevated cholesterol ester levels e.g. hypercholesterolemia
                                                                                                                                         Human acyl CoA:cholesterol acyltransferase 2 antisense PCR primer.
                                                                                                                                                                               Human; acyl CoA:cholesterol acyltransferase; ACAT-2; diagno
antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 21; Length 20;
Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erickson SK;
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100.0%; P.
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                                                                                                                                                                                                                           hyperlipidaemia; PCR primer; ss
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99US-0328857
                  AAZ57364 standard; DNA; 20
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                                                                                                  05-APR-2000 (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA
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08-JUN-1999;
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                                                            AAZ57364;
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  AAZ57364/C
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COA:cholesterol acyltransferase designated ACAT-2. ACAT-2 polypeptides
Can be administered therapeutically, especially by expressing encoding
polynucleotides, to treat individuals in need of ACAT-2 polypeptide.
They may especially be administered to treat disease conditions
associated with elevated cholesterol ester levels e.g.
hypertholesterolaemia or hyperlipidaemia (including
hypertholesterolaemia) since ACAT-2 catalyses the esterification of
cholesterol with fatty acyl CoA substrates. The polypeptides can also
be used to dispnose diseases related to polypeptide expression or
activity, by analysing for polypeptide presence or amount in a sample.
They are useful to screen for compounds inhibiting or activating the
polypeptide, which can be included in pharmaceutical compositions and
administered therapeutically to treat conditions associated with ACAT-2;
thibitory agents can especially be used to inhibit ACAT-2 activity,
chitit accent.
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  Gaps
                                                                                                                                                                                                                                                                                                                                            Human; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis;
antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;
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                                                                                                                                                                                                                                                                                                    Human acyl CoA:cholesterol acyltransferase 2 sense PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erickson SK;
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  0; Mismatches
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                                     1539 GACACCTCGATCTTGGTCCTGCC 1561
                                                                                                                                                                                                                                                                                                                                                                                   hyperlipidaemia; PCR primer; ss.
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                                                          1 GACACCTCGATCTTGGTCCTGCC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1331 TCTTCTATCCGTCATGCTG 1350
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99US-0328857
                                                                                                                                                                             AA257363 standard; DNA; 20
                                                                                                                                                                                                                                                              (first entry)
  Conservative
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Matches 20; Conserv
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08-JUN-1999;
23;
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Cases S,

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Gaps

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Query Match

RESULT

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Rat spliced transcript detection oligonucleotide SEQ ID NO:1510.

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AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA269579 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; Ig; heavy chain; stimulation; inhibition; treatment; IgM; IgG; IgA; IgE; isotype switching; allergy; autoimmune; alloimmune.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing
                                            genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                       Human genome; biallelic marker; high density disequilibrium map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 16; DB 21; Length 20; 00.0%; Pred. No. 2.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 2731; 2745pp; English.
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TCCTCTTGCCCAAC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         map of the human genome
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                                                                                                                                          diagnosis; ss
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23-NOV-1998;
                                                                                                                                                                                                                                                                                                              28-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
AAV21372
δž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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Condition, to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a particular disorder. ABNZ7251 to ABNS9589 represent

Condition of the present invention.

Che exemplification of the present invention.

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Che exemplification of the present invention of the printed for this patent for that patent for this patent for man and the present invention the present invention the present invention that the properties of the present properties of the printed for this patent for the printed for this patent for the printed for the printe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human biallelic marker downstream amplification primer SEQ ID NO:11729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                          Human; mouse; rat; splice transcript; detection; RNA transcript;
splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65 BP; 17 A; 24 C; 8 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoshan A, Wasserman A, Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID 1510; 47pp; English.
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Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                      20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ77373 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-257383/30.
                                                                                                                     Rattus norvegicus
                                                                                                                                                                       WO200210449-A2.
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from human breast for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label carled from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents after greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Where the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/published_pct_sequences.
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                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon
                                                                                             New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                             Claim 4; SEQ ID NO 9236; 327pp + sequence listing; English.
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00.0%; Pred. No. 2.3e+03;
.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #16805.
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                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
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                   Chen W,
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 16; Conservative
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                   Hanzel DK,
                                                    WPI; 2001-496933/54.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                SG,
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                   Penn
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                                                                                                                                                                                                                                                                                                                                                                       The nucleotides AAV21362-V21373 are examples of the genomic fragments from which sequences were used to create trans-spliced transcripts. The transcripts competize a sequence capable of annealing to a human genomic immunoglobulin (Ig) heavy chain I region of a locus selected from mu, epsilon, alpha and gamma followed by a second sequence capable of annealing to a region of a second locus selected from mu, epsilon, alpha and gamma as above. The products can be used for stimulating or inhibiting synthesis of a particular human Ig isotype. They can be used for treating disorders mediated by IgM, IgG, IgA or IgE, in particular for inhibiting IgE synthesis or isotype switching to IgE for treating allergic disorders. They can also be used for treating autoimmune and alloimmune diseases amongst others.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                       New immunoglobulin trans-spliced transcripts - used for, e.g. stimulating or inhibiting synthesis of particular immunoglobulin isotype, useful for treating immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0%; Score 16; DB 19; 0.0%; Pred. No. 2.3e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60 BP; 16 A; 8 C; 30 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                         Example 2; Page 36; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0°,
100.0%; Pre-
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2000US-0234687.
2000US-0236359.
                                                                                                                                                                             Ke Z, Saxon AW;
                                                    97WO-US15485
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2000US-0608408.
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                                                                                             96US-0023579
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Matches 16; Conservative
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                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                   WPI; 1998-179050/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157271-A2
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26-MAY-2000;
30-JUN-2000;
                                                    15-AUG-1997;
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              26-FEB-1998
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                                                                                                                                                                           Fujieda S,
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ABA50541
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                 Query Match
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                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                    Probe #13947 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                    Claim 4; SEQ ID NO 16805; 639pp + sequence listing; English.
                                                                                                                                                                                                    Length 87;
                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                   Score 16; DB 22; | Pred. No. 2.3e+03;
                                                                                                                                                                                Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
                                                                                                                                                                                                          100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                       ABA35481 standard; DNA; 87 BP
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                   Query Match 1.0 Best Local Similarity 100. Matches 16; Conservative
                                                                                                                                                                                                                                             134 TGGAGGCTGTGAAGGC 149
                                                                                                                                                                                                                                                           TGGAGGCTGTGAAGGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488899/53
 WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157274-A2.
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                23-JAN-2002
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                                                            system
                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systementials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                       e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 16858; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                           Length 87;
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                                                                                                                                                                                                                                                      Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                              1.0%; Score 16;
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100.0%;
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         134 TGGAGGCTGTGAAGGC 149
                                                                                                                    congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy; cancer; ss
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tes 16; Conserv
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27-SEP-2000;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
   Probe #13325 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #17401 used to measure gene expression in human placenta sample.
                                     human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful fanalyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; microarray; human; placenta; antenatal diagnosis;
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100.0%; Pred. No. 2.3e+03;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID No 13325; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Rank DR
                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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26-MAY-22000, 2000US-0207456.
30-UJN-2000; 2000US-060B408.
03-AUG-2000; 2000US-023366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TGGAGGCTGTGAAGGC 20
                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488901/53.
                                                      cervical cancer; ss
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Best Local Similarity
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                                                                                        Homo sapiens
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                                     Probe;
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   Gaps
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                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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100.0%; Pred. No. 2.3e+03;
lve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
 Mismatches
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100.0%; Prt
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
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                                 134 TGGAGGCTGTGAAGGC 149
16; Conservative
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nes 16; Conserv
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30-JUN-2000;
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AAI23392
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Gaps

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Length 87; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 17401; 654pp; English.
                                                                                                                                                                                                            Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                              04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0668408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
30-JAN-2001; 2001WO-US00663.
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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 20801, A		16,	Sequence 4, Appli	C	Sequence 25, Appl	Sequence 8, Appli	18	Sequence 104, App	Sequence 6, Appli	24	Sequence 3227, Ap	Sequence 24518, A	Sequence 1141, Ap	Sequence 1141, Ap	Sequence 26, Appl			Sequence 12594, A	
QI.	US-09-864-761-20801	US-09-854-883-174	US-09-775-925-16	US-09-801-274-4	US-09-898-323-20	US-09-919-060-25	US-09-292-973-8	US-09-898-541-18	US-09-815-837-104	US-09-785-632A-6	US-09-898-323-24	US-09-878-574-3227	US-09-864-761-24518	US-09-920-300A-1141	US-10-033-528-1141	US-09-853-666-26	US-09-864-761-23349	US-09-815-242-3561	US-09-878-574-12594	
08	10	10	10	10	10	10	10	10	10	10	10	10	10	10	12	10	10	10	10	
% Query Match Length DB	87	20	25	31	51	24	25	30	36	47	47	68	82	88	88	90	86	98	86	
% Query Match	1.0	1.0	1.0	1.0	1.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	0.9	6.0	
Score	16	15	15	15	15	14	14	14	14	14	14	14	14	14	14	14	14	14	14	
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equence 2593, Ap equence 2294, Ap equence 2295, Ap equence 2295, Ap equence 2297, Ap equence 9, App11 equence 9, App11 equence 25, App1 equence 27, App1 equence 329, Ap equence 5223, Ap equence 5224, Ap equence 5226, Ap	ACID PROBES USEFUL	
	HY MICELEIC	
S. 09-815-242-35 S. 09-866-108-22 S. 09-866-108-22 S. 09-866-108-22 S. 09-866-108-22 S. 09-866-108-22 S. 09-967-624-16 S. 09-967-624-16 S. 09-967-624-16 S. 09-87-528-50 S. 09-817-31-32 S. 09-817-31-32 S. 09-817-31-32 S. 09-818-32-32 S. 09-866-108-52 S. 09-866-108-52	S SINGI	FILE REFERENCE: Aeomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR PELLOR DATE: 2000-05-04 PRIOR PELLING DATE: 2000-05-06 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-08-03 PRIOR PELING DATE: 2000-09-03 PRIOR PELING DATE: 2000-09-03 PRIOR PELING DATE: 2000-09-07 PRIOR PELING DATE: 2000-09-07 PRIOR PELING DATE: 2000-09-07 PRIOR PELING DATE: 2001-01-30
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91111111111111111111111111111111111111	ication (8763A1 arron G. avid R. David K ensheng HUMAN GI	DN NUMBER: 2001-01-01-01-01-01-01-01-01-01-01-01-01-
	301 APPL 302004 ATION: 307, Sh ank, D anzel, W ATION:	TEL AGO (CATION OF AGO MICHON IN DATE: MICHON IN DATE: MICHON IN M
48888888888888888888888888888	4-761-206 ce 20801, No. US20 L INFORM CANT: Per CANT: He CANT: He CANT: CI OF INVER	REFERENCE: Aeomica-X INT APPLICATION NUMBER PELLING DATE: 2000-0 APPLICATION NUMBER: FILING DATE: 2001-0 APPLICATION NUMBER:
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	REGIONAL CONTRACTOR CO	

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APPLICANT: Cargill, Michele
APPLICANT: Lander, Eric S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FRASED for Windows Version 4.0
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; Pred. No. 6.9e+02;
0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                    FILE REFERENCE: 200125.420
CURRENT APPLICATION NUMBER: US/09/775,925
CURRENT FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.06
SEQ ID NO 16
LENGTH: 25
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Pred. No.
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100.0%; Pre
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                                                                                                                      Sequence 16, Application US/09775925 Patent No. US20010049358A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09801274 Patent No. US20020032319Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                   20 IGCCCCCACCICCCC
US-09-775-925-16/c
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SEQ ID NO 4
LENGTH: 31
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APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Medeline M. Butler
APPLICANT: Medeline M. Butler
APPLICANT: Mobert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
CURRENT APPLICATION NUMBER: US/09/854,883
CURRENT PILING DATE: 2001-05-14
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 174
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                     N: EXPRESSED IN FETAL LIVER, SIGNAL = 8.5
NN: EXPRESSED IN ADULT LIVER, SIGNAL = 9.6
NN: EXPRESSED IN BONE MARROW, SIGNAL = 8.5
NN: EXPRESSED IN HELA, SIGNAL = 8.4
NN: EXPRESSED IN HELA, SIGNAL = 8.4
NN: EXPRESSED IN HELAO, SIGNAL = 8.7
NN: EXPRESSED IN LUNG, SIGNAL = 8.7
NN: EXPRESSED IN LUNG, SIGNAL = 9.4
NN: EXPRESSED IN HEART, SIGNAL = 7.2
NN: EXPRESSED IN HEART, SIGNAL = 7.7
NN: EXPRESSED IN HEART, SIGNAL = 7.7
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CTHER INFORMATION: SWISSPROT HIT: P80152, EVALUE 7.10e+00
CTHER INFORMATION: EST_HUMAN HIT: R09942.1, EVALUE 1.00e-17
US-09-864-761-20801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20801
LENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16;
Pred. No.
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PELLOATION NUMBER: US 60/234,687
PRIOR FLILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELLOATION NUMBER: US 09/774,203
PRIOR PELLOATION NUMBER: US 09/774,203
APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                      TO AL022308.1
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Patent No. US20020055479A1
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100.0%; Pre
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Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserva
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OTHER INFORMATION:
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INFORMATION:
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                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:primer US-09-292-973-8
                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 30;
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TITLE OF INVENTION: Method and Reagents for Genetic
Immunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
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. 2.2e+03;
ches 0;
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2.2e+03;
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REGISTRATION NUMBER: 32,038
REFRENCE/DOCKET NUMBER: MSK.P-012
TELECCMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
                                                                                                                                                                                                                Query Match 0.9%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 14; DB
100.0%; Pred. No. 2.2
ative 0; Mismatches
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FILING DATE: 02-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 18
US-09-898-541-18
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FILING DATE: <Unknown>
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ADDRESSEE: Oppedahl & Larson
STREET: PO BOX 5270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Houghton, Alan
Bartido, Shirley M.
Xu, Yiquing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09898541
Patent No. US20020072504A1
GENERAL INFORMATION:
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TELEX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 18:
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                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 25
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                6 IGCIGCIGCICAIC 19
    NUMBER OF SEQ ID NOS: 20
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STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
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US-09-898-541-18/c
                                                                                       TYPE: DNA
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APPLICANT: Wisnewski, Nancy
APPLICANT: Wisnewski, Nancy
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
TILE REPRENCE: AD-1
CURRENT APPLICATION NUMBER: US/09/919,060
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTION NUMBER: OF SEQ ID NOS: 25
LENGTHARE: PATENTION STATEMENT OF SEQ ID NOS: 25
LENGTH: 24
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APPLICANT: MCWHINNIE, Elizabeth A.
TITLE OF INVENTION: No. US20020111473A1e1 G Protein Coupled Receptor PILLE REPERENCE: 8074-9004
CURRENT APPLICATION NUMBER: US/09/292, 973
CURRENT FILING DATE: 1999-04-16
EARLIER APPLICATION NUMBER: US 60/081, 995
EARLIER FILING DATE: 1998-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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             APPLICANT: Livak, Kenneth J.
APPLICANT: Livak, Kenneth J.
APPLICANT: Bloch, Will
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE ASSAY
FILE REFERENCE: 4559US
CURRENT APPLICATION NUMBER: US/09/898,323
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/216,514
PRIOR PILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
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0.9%; Score 14; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 15; DB 10;
100.0%; Pred. No. 7e+02;
Live 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Synthetic Primer US-09-919-060-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09919060
Patent No. US20020064845A1
GENERAL INFORMATION:
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Patent No. US20020111473A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.0
Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT: Bi, Wanli
                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             us-09-919-060-25/c
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                                                                                                                                                                                                                                  SEQ ID NO 20
LENGTH: 51
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Query Match 0.99
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                            15 AGCCGCCCACGCCG
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ORGANISM: Unknown
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US-09-878-574-3227
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LENGTH: 68
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Sequence 6, Application US/09785632A
Patent No. US20020061512A1
GENERAL INFORMATION:
APPLICANT: Kim, Jin-So
APPLICANT: Kim, Hyun-Won
APPLICANT: Kim, Hyun-Won
APPLICANT: Ryu, Eun-Hyun
APPLICANT: Hwang, Moon-Sun
TITLE OF INVENTION: IDENTIFYING SAME
TITLE OF INVENTION: IDENTIFYING SAME
FILE REFERENCE: 1279-002001
FILE REFERENCE: 2279-002001
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 166
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 47
                                                                                                                                                                                                                                                   APPLICANT: Caller, Shirley
APPLICANT: Arimili, Subhashini
APPLICANT: Arimili, Subhashini
APPLICANT: Wang, Aljurey
APPLICANT: Wang, Aljurey
APPLICANT: Wang, Aljurey
APPLICANT: Wang, Aljurey
APPLICANT: Corporation
TITLE OF INVENTION: Immune Medators and Related Methods
FILE REFERENCE: 014058-005670US
CURRENT APPLICATION NUMBER: US 60/191,274
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 104
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0.9%; Score 14; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0;
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                                                                                                                                                                  ; Sequence 104, Application US/09815837; Patent No. US20020082411A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Carter, Darrick
APPLICANT: Zhu, Shirley
APPLICANT: Arimilli, Subha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 AGCCGCCCACGCCG 625
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             763 CTTCGTGCCAGACG 776
                                       15 CTTCGTGCCAGACG 2
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US-09-785-632A-6/c
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US-09-815-837-104
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CTHER INFORMATION: Ligation product of probes Ap3 and Ap4 from Scheme IIb, follow contex INFORMATION: cleavage of Ap4 US-09-898-323-24
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Sequence 3127, Application US/09878574

GENERAL INFORMATION:

SAPPLICANT: Byrun, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT PAPLICANTON: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION UNMER: 09/333,535
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Length 47;
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                                              Indels
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US-09-698-323-24

Sequence 24, Application US/09898323
Sequence 24, Application US/09898323
Sequence 24, Application US/09898323
Setent No. US20020150904A1
GENERAL INFORMATION:
APPLICANT: Bi, Wanli
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE ASSAY
TILE REFERENCE: 4559US
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/216,514
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 24
LENGTH: 47
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0.9%; Score 14; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0;
  0.9%; Score 14; DB 10; 1
100.0%; Pred. No. 2.3e+03;
tive 0; Mismatches 0;
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                                                                                              612 AGCCGCCCACGCCG 625
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Gaps

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Indels

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GENERAL INPORMATION:
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Madeleine Joy
APPLICANT: Au, Jiangchun
APPLICANT: Au, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1141.88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1141, Application US/10033528
Sequence 1141, Application US/10033528
Patent No. US20020131971a1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Scrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1141
Pred. No. 2.3e+03;
; Mismatches 0;
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100.0%; Pred. No. 2.3e+03;
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100.0%; Pred. No. 2.3e+03;
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        100.0%;
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                      32 GTGGAGATGGAAAC 45
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                                                                                         74 GTGGAGATGGAAAC
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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US-09-920-300A-1141
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                                                                                                                                                                                                             APPLICANT: Penn, Sharren G.
APPLICANT: Penn, Sharren G.
APPLICANT: Penn, Sharren G.
APPLICANT: Penn, Sharren G.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aconica X-1
CURRENT FILING DATE: 2001-05-20
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-01-30
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N: EXPRESSED IN PLACERTA, SIGNAL = 1.3
N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
N: EXPRESSED IN HELA, SIGNAL = 2.7
N: EXPRESSED IN HEART, SIGNAL = 1.5
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
N: EXPRESSED IN LUNG, SIGNAL = 1.3
N: EXPRESSED IN BRAIN, SIGNAL = 1.4
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 24518
TENEMAL R.
                                                                                RESULT 13
US-09-864-761-24518
Sequence 24518, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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27 ATGCTGGGTGTGTT 40
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ORGANISM: Homo sapiens
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Gaps

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Indels

Length 88;

Search completed: November 14, 2002, 20:57:26 Job time: 73 secs

Score 14; DB 10; Length 82;

0.98;

Query Match

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Gaps

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Indels

Length 88;

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Perfect score:

Sequence:

OM nucleic

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Scoring table:

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Minimum DB Maximum DB

Database :

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AU10553 AU105503
AI826950 wk57c01.x
A289723 1M0150J10
BE041235 hk46d11.y
BE043557 hk40b06.y
BE043527 hk36d11.y
BE043859 hk44e12.y
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BE043552 hk40b01.y
BE043531 hk39906.y
BF055887 7i75a09.y
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BE042163 hk34a08.y
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BE043561 hk40b10.y
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A1324031 qv51601.x
A1324331 m109h05.x
A1336731 qw99912.x
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A133631 qw86c01.x
A140813 tb54608.x
A1240840 qx22a10.x
A1250596 qx22h12.x
A1250596 qx22h12.x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walbot,V. Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                         AI223491 qx27c06.x
BI676290 1b80b02.x
T10503 hbc575 Huma
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 71)
                              BI175453 OSTR046A5
                   B39146 HS-1049-A1-
                                                                                                                                                                                                                       AI197018 ue47h04.r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Very probable ligation site of ends cut by a single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 1006021 row: 38 Class: transposon-tagged. Location/Qualifiers
                                                 AU105500 AU105500
AU105502 AU105502
AU105502 AU105502
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[006021F08.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotéstanford.edu
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BE042163
BE043435
BE043431
A1223491
B1076290
T10503
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A1336711
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KEYWORDS
SOURCE
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TITLE
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AZ920873 1006021F0
F31995 HSPD23742 H
BL472373 fs02d01.y
AA791480 vs66f11.r
F74292 HSPD10465 H
BH850932 SALK_0721
                                                                              (without alignments)
13603.168 Million cell updates/sec
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                                                                                                                             1 atggagccaggcggggcccg........ttggtcctgccatacctag 1569
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                                                                 November 14, 2002, 19:27:46; Search time 1868 Seconds
                                                                                                                                                                                                                       357874
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                              16154066 segs, 8097743376 residues
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                        summaries
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F31995
B1472373
AA791480
F24292
BH850932
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Gapop 60.0 , Gapext 60.0
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em_gss_pro:*
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Gaps

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i (bases I to 89)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hillier, L., Rucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Hillier, L., Theislag, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Mshul Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                f502d01.y1 Zebrafish adult olfactory Danio rerio cDNA clone 5002416 b1472273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: John Ngai CDNA Library Arrayed by:

CDNA Library Preparation: John Ngai CDNA Library Arrayed by:

Atthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@qenomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarbatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Olfactory rosettes"
/dev_stage="adult"
/lab_host="DlOHD (Gibco BRL)"
/note="Vector: psPoRT1; Site_1: Not1; Site_2: Sal1; This is a directionally cloned cDNA library from adult
Zebrafish olfactory epithelium."
streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector." 20\ c 25\ g 10\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 89;
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100.0%; Pred. No. 2.6e+03;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.6e+03;
iive 0; Mismatches 0;
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/db_xref="taxon:7955"
/clone="5002416"
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JOURNAL
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BI472373
LOCUS
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KEYWORDS
SOURCE
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                                                                                                                                                                                          /noce="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.ramb.iastate.edu' and follow the links for 'RescueMu', Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 bp mRNA linear EST 13-MAY-1999
F31995
F31995.1 GI:4817621
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
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0
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                                            /organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
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/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
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100.0%; Pred. No. 2.5e+03;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="s4000089G03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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CRIBI Biotechnology Centre
University of Padua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="HM3"
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Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,
Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligo-dT-NotI primer (5'-biotin-AACCCGGCTCGACGCCGCTTTTTTTTTTTTTTTTT-3'). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alonso, J. W., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Stle_2: Stle_2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector." 27 c 26 g 11 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to
                                                                                                                                                                                                                                                   Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW
http://grup.bio.unipd.it.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH850932 74 bp DNA linear GSS 13-; SALK_072110.31.45.x Arabidopsis thaliana TDNA insertion line Arabidopsis thaliana genomic clone SALK_072110.31.45.x, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pectoral muscle (after mastectomy)"
      Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
T=1: 858 453 4100 x1752
Fax: 858 558 6379
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Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                      1. .93
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000006H09"
/clone_lib="HM3"
                                                                                                                                                                                      Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Sco.
100.0%; Pre
0;
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Arabidopsis thaliana
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F24292
F24292.1 GI:4809918
EST.
                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 91)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelalang,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                      vs66f11.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1151277 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="InMAGE:1151277"
/clone=lib="Stratagene mouse skin (#937313)"
/sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17; DB 9; Length 91;
Pred. No. 2.7e+03;
0; Mismatches 0; Indels
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Location/Qualifiers
1. .91
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/strain="C57BL/6"
                                                                                                                                                                                      AA791480.1 GI:2854435
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100.0%;
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Best Local Similarity 100.
Matches 17; Conservative
62 CATGGAGGCTGTGAAGG 78
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                                                                                                                                                                                                                                  house mouse.
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                                                                                                                                                                     AA791480
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F24292/C
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Length 93; Indels 13-JUN-2002 lines

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BH417282
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B 1 (bases 1 to 76)

S Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Context: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                          /strain="Columbia 0"
/db_xref="taxon:3702"
/clone="salk_072110.31.45.x"
/clone="lb="hazhaldopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of Which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 20 c 17 g 15 t
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             This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3954900 Class: TDNA tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 16; DB 17; Length 74; 100.0%; Pred. No. 8e+03; Ve 0; Mismatches 0; Indels
                                                                                                         1. .74
/organism="Arabidopsis thaliana"
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100.0%; Preα. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error
Plate: 0025 row: B column: 16
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/clone="UUGC2M0025B16"
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                                                                              Location/Qualifiers
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Email: ecker@salk.edu
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Fax: 801 585 7177
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AZ783832/c
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the lineart adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 12-DEC-2001
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 88)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 650 725
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Peverse complemented post-ligation sequence from source sequence.
Plate: 1007053 column: 17
Class: transposon-tagged.
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1007053G01.y1 1007 - RescueMu Grid H Zea mays genomic, DNA
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/cultivar="mixed background W23/A188/B73"
/db xref="taxon:4577"
/clone_lib="lon07 - RescueMu Grid H"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
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8.1e+03;
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llarity 100.0%; Pred. No. 8.1
Conservative 0; Mismatches
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es 16; Conserv
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EUKATYOCIS, Metazos: Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases i to 100)

1 (bases i to 100)

Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hittly, Duccette-Stamm, L., Hartley, J.L., Temple, G.F., Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans

Nat. Genet. 27 (3), 332-336 (2001)
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36 bp DNA linear GSS 05-OCT-2000
1M0326005F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0326005 F, DNA sequence.
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/clone_lib="AD-wrmcDNA"
/clone_lib="AD-wrmcDNA"
/tssa="meaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+
RA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Jerome_Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans O
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
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100.0%; Pred. No. 8.6e+03;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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1. .100
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      BI175453.1 GI:14641256
                                          Caenorhabditis elegans.
Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 91)
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,
Traitoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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/clone_lib="CIT Human Genomic Sperm Library C"
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                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Mahalaras GG, Zackrone KD, Hood L.
Contact: Mahalaras GG, Zackrone KD, Hood L.
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 665-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 771 row: K column: 17
Class: BAC ends
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8.3e+03;
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8.4e+03;
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/db_xref="taxon:9606"
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ilarity 100.0%;
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B39146/c
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Contact: Yutaka Suzuki
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1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/db_xref="taxon:10090"
/clone="upcZlw0326005"
/clone_lib="Mouse 10kb plasmid UUGClM library"
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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Location/Qualifiers
                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 5td Erro
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100.08; Pre-
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
5-6-1, Shirokanedai, Minatcku, Tokyo ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama, K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library, Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
Department of Virology Institute of Medical Science, University of Tokyo Institute of Medical Science, University of Tokyo B619, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki%i.y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Guyama,A. and Sugano so. S. construction and characterization of a full length-enriched and so. S. cond-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AULOSSOU Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC12477, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRc07611"
/clone="Lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
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Pred. No. 2.3e+04;
0; Mismatches 0;
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Pred. No. 2.3e+04;
0; Mismatches 0;

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    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/clone_lib="Sugano Homo
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EMBO Rep. 2 (5), 388-393 (2001)
21270072
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Best Local Similarity 100.
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Search completed: November 14, 2002, 20:54:33
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiélms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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EMBO Rep. 2 (5), 388-393 (2001)
                                                                                             AU105502 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AVI00558, mRNA sequence.
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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 50)
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Pred. No. 2.3e+04;
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/db_xref="taxon:9606"
/clone="KAT00658"
/clone_lib="Sugano Homo s
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AU105502.1 GI:13555023
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AU105503.1 GI:13555024
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Matches 15; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                        RESULT 14
AU105502/c
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuukikilms.u-tokyo.ac.jp
Email: ysukikilms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo.Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT04851"
/clone=lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
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100.0%; Pred. No. 2.3e+04;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 15; Conservative
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Query Match
Best Local Similarity
; TYPE: DNA
; ORGANISM: human
US-09-165-042-30
0000000000000000
                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: human
US-09-165-042-25
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US-09-165-042-30
LENGTH: 25
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Sequence 171, App
Sequence 37, Appl
Sequence 38, Appl
Sequence 283, App
Sequence 283, App
Sequence 283, App
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
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54, Appl
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                                                                  (without alignments)
7888.129 Million cell updates/sec
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1 atggagccaggcgggggccg..................ttggtcctgccatacctag 1569
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                                                        November 14, 2002, 19:30:01; Search time 61 Seconds
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       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-974-549A-683
US-08-985-162-144
US-09-487-368A-174
US-09-676-610B-171
US-09-676-610B-171
US-08-482-182-36
US-08-411-796-283
US-08-471-039-283
US-08-584-040-4455
PCT-US93-11198-283
US-08-81-50-54
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-08-758-306-1166
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US-08-890-980-84
US-09-032-894-84
US-09-031-626-84
US-09-255-368-13
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US-08-998-099-231
US-09-417-822-19
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                                                                                                                                                      441362 segs, 153338381 residues
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                                        nucleic search, using sw model
                                                                                                                            OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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                                                                                            US-09-918-026A-3
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Match Length
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seq length: 100
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Sequence 18, Appl
Patent No. 5401629
Sequence 286, App
                                                                   Sequence 36, App]
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Sequence 15,
Sequence 337,
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Sequence 25, Application US/09165042

Sequence 25, Application US/09165042

Patent No. 6100077

GENERAL INFORMATION:
APPLICAMT: Sturiey, Stephen L.
APPLICAMT: OSLATION STORE STURIES OF TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
TITLE OF INVENTION: ACYLTRANSFERASE
FILE REFERENCE: 0575/5631

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6100077

GENERAL INFORMATION:
APPLICANT: Sturiey, Stephen L.
APPLICANT: Oelkers, Peter
TILLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
TILLE OF INVENTION: ASOLATION OF A GENE ENCODING DIACYLGLYCEROL
TILLE REPERENCE: 0575/56331
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 30
LENGTH: 23
LENGTH: 23
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100.0%; Pred. No. 0.052;
ive 0; Mismatches 0; Indels
                     5175384-4

US-09-996-338-36

US-09-230-199-18

5401629-1

US-08-943-336A-15

US-08-943-336A-15

US-08-943-336A-15

US-08-363-240A-864

US-08-363-240A-865

US-08-363-240A-865

US-08-363-240A-865

US-08-868-865

US-08-868-865

US-08-898-881-20

US-08-808-881-20

US-08-93-674A-66
PCT-US93-11198-282
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1.0%; Score 16; DB 4; Length 89; 100.0%; Pred. No. 3.2e+02; 1ve 0; Mismatches 0; Indels
                                              Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION UNBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997 CLASSIPICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/R<sup>51</sup> 0.7
FILING NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
PRIOR DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0%; Sco
Best Local Similarity 100.0%; P:
Matches 16; Conservative 0;
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
ITILE OF INVENTION: Human Telon
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..89
OTHER INFORMATION:
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                                                                                                                                                                                                      COUNTRY:
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                           ;
0
                                                                                                                                                                                                                Sequence 67, Application US/08911894
Patent No. 6030830
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Tahng, Ke
APPLICANT: Thisda, Shigeharu
TITLE OF INVENTION: IMMUNOGLOBULIN TRANS-SPLICED TRANSCRIPTS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 16; DB 3; Length 60; 100.0%; Pred. No. 3.3e+02;
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                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TENDANG LE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TENDANG LE FORMS:
COMPUTER: TENDANG LE FORMS:
COMPUTER: TENDANG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,894
FILING DATE: CONCULTENTLY HERWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/023,579
FILING DATE: 19-AUG-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAY/AGENT INFORMATION:
NEGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: 43496.0006
TELECOMMUNICATION INFORMATION:
METERRENCE/DOCKET NUMBER: 43496.0006
TELECOMMUNICATION INFORMATION:
METERRENCE/DOCKET NUMBER: 43496.0006
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816 Congress Avenue, Suite 1900
      0.15;
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      Pred. No.
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                                                                       1539 GACACCTCGATCTTGGTCCTGCC 1561
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100.0%; Pi
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    ilarity 100.0%; P. Conservative 0;
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (512) 499-6200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBERHOUSE. (512) 499-6290
INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
      Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ACCIONATE: Texas COUNTRY: USA 78701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-08-974-549A-683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-911-894-67
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Gaps ; 0

Length 90;

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APPLICANT: ARMER, Saghir
APPLICANT: Fell, Parricia
APPLICANT: McSwigen, James APPLICANT: MCSWIGEN APPLICANT TITLE OF INVENTION: TO LEVELS OF EPIDERWAL GROWTH TITLE OF INVENTION: TO FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Los Angeles
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                       ; NAME/KEY: -
; LOCATION: 1..90
: OTHER INFORMATION: /note= "oligonucleotide 211"
US-08-974-549A-684
                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 16; DB 4; L
100.0%; Pred. No. 3.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLUGY RICHARD J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 15;
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 144, Application US/08985162 Patent No. 6057156
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 144:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 CTTCAGCTTCGGACAG 486
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.0
Best Local Similarity 100.
Matches 16; Conservative
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LENGTH: 17 base pairs
TYPE: nucleic acid
INFORMATION FOR SEQ ID NO:
                                                     LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 CTTCAGCTTCGGACAG 28
                            SEQUENCE CHARACTERISTICS
                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: COMPUTER: COMPUTER
                                                                                                                                                                                                                                 Sequence 684, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
ELECOMMUNICATION INFORMATION
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TELEFAX: (415) 576-0300
               STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                 US-08-974-549A-684/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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ATTORNEY/AGENT INFORMATION: 'NAME: PARK, FREDDIE K.
OLSON, PAMELA S.
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CITY: Palo Alto
STATE: California
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                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                       94304-1018
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US-08-482-182-36/c
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US-08-482-182-37
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 APPLICANT:
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                     Gaps
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GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
APPLICANT: Susam M. Freier
TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
                                                                                                                                                                                                                      APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION UMBER: US/09/487,368A
CURRENT APPLICATION UMBER: US/09/487,368A
CURRENT FILING DATE: 2000-01.18
SEQ ID NO 174
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 15; DB 4; Length 20; 100.0%; Pred. No. 1e+03;
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                       Indels
     Pred. No. 1e+03;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ), OTHER INFORMATION: Antisense Oligonucleotide US-09-487-368A-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. +ive 0; Mismatches
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CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 171
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-676-610B-171
; Sequence 171, Application US/09676610B
; Patent No. 6444465
                                                                                                                                               US-08-482-182-37; Sequence 37, Application US/08482182; Sequence 37, Application US/08482182; Patent No. 5861273; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MASCARENHAS, DESMOND
     Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.0
Best Local Similarity 100.
Matches 15; Conservative
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                                                          340 CTGATGGAGGTGCAG 354
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                                                                               15 CTGATGGAGGTGCAG 1
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                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Patent No. 5861273
CENERAL INFORMATION:
APPLICANT: MASCARENHAS, DESMOND
APPLICANT: OLSON, PAMELA S.
TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS TITLE OF INVENTION: GRES IN BACTERIAL CELLS
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSED: MORRISON & FORESTER
STREET: 755 Page Mill Road
CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
GENES IN BACTERIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 76;
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7. 9.7e+02;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,182
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,182
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ...
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100.0%; Pred. No.
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                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 705141
                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1059 CATCTTCTTTGCCTT 1073
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Best Local Similarity 100.0
Matches 15; Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                              Abba...
STREET: 755 ...
CITY: Palo Alto
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APPLICANT: Polazzi, Joseph O.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
NUMBER OF SEQUENCES: 549
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          0.9%; Score 14; DB 1; Length 18; 100.0%; Pred. No. 3e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC COMPUTER:
COMPUTER: DATHER: DATHER: US/08/471,039
FLING DATE: 06-JUN 1995
FLING DATE: 06-JUN 1995
FILING DATE: 24-NOV-1992
PRICH APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
PRICH APPLICATION NUMBER: PCT/US93/11198
FILING DATE: 22-NOV-1993
ATTONEY/AGENT INFORMATION:
WANTER TABLES THE POSMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Dennis A. Bennett, G.D. Searle & Co.
E: Corporate Patent Dept.
P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Braford-Goldberg, Sarah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 283, Application US/08471039
; Patent No. 6017523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 283: SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-411-796-283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (synthetic) US-08-471-039-283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caparon, Maire H.
Easton, Alan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein, Barbara K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MCKearn, John P. APPLICANT: Olins, Peter O. APPLICANT: Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
                                                                                                                                                                                                  Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                     1548 ATCTTGGTCCTGCC 1561
                LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                             1 ATCTTGGTCCTGCC 14
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-471-039-283
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                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: McKear, John P.
APPLICANT: Olins, Peter O.
APPLICANT: Palaz, Kunnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
NUMBER OF SEQUENCES: 549
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                        Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co. ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,796
                                                                                                                                                                                                                                                                                                                                Query Match 1.0%; Score 15; DB 2; Les Best Local Similarity 100.0%; Pred. No. 9.7e+02; Matches 15; Conservative 0; Mismatches 0;
                                   22095-20281.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/981044
FILING DATE: 24-NOV-1992
PRIOR APPLICATION NUMBER: PCT/US93/11198
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C2713/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 283, Application US/08411795
Patent No. 5677149
GENERAL INFORMATION:
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 22095
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEEX: 706141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 283:
                                                                                                                                                                                                                                                                                                                                                                                                                              1059 CATCTTCTTTGCCTT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 CATCTTTGCCTT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60680
                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-482-182-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-411-796-283
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981044
FILING DATE: 24-NOV-1992
ATTORNEY/AGENT INFORMATION:
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REFRENCE/COCKET NUMBER: C2713/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bennett, Dennis A REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1548 ATCTTGGTCCTGCC 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-851-520-54/C
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                                         ö
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
0.9%; Score 14; DB 3; Length 18;
100.0%; Pred. No. 3e+03;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                    RESULT 13
US-08-564-040-4455

Sequence 4455, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Bavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: CALOUR TREAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

SOFTWARE: WORD PEFCET 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14;
Pred. No.
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APPLICATION NUMBER: 60/005,974
FILING DATE: 00ctober 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,337
REFERENCE/DOCKET NUMBER: 218/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 0.9
Best Local Similarity 78.6
Matches 11; Conservative
  Query Match 0.9
Best Local Similarity 100.
Matches 14; Conservative
                                                                                    1548 ATCTTGGTCCTGCC 1561
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                                                                                                          1 ATCTTGGTCCTGCC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-584-040-4455
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Sequence 54, Application US/09851520
Patent No. 6399379
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0241
CURRENT APPLICATION NUMBER: US/09/851,520
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 54
LENGTH: 20
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APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Braford Solution Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Paik, Kumnan
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                             ADDRESSE: Dennis A. Bennett, G.D. Searle & CO., ADDRESSE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 14; DB 5; Ler
100.0%; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. no.
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; FEATURES:
; COTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-54
Query Match
Guery Match
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps
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0;

Search completed: November 14, 2002, 20:55:54 Job time: 63 secs

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(OTASU) ANAJA 39A9 SIHT